

and high vitamin D levels ($P < 0.001$) are strongly associated with SVR.

Conclusions: Low serum HDL and high vitamin D levels are strongly associated with sustained viral response in chronic HCV naïve genotype-1 patients.

PP-131 Screening of proteins binding to hepatitis C virus NS4B protein from human pancreas cDNA library

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Objective: To screen gene encoding of pancreatic proteins from human pancreas cDNA library, which interact with hepatitis C virus (HCV) NS4B protein.

Method: The human pancreas cDNA library was amplified, purified and evaluated, and the purified library plasmids were transformed into yeast strain Y187. The reconstructed plasmid pGBKT7-NS4B was transformed into yeast strain AH109 and the positive colonies were screened on the nutrient deficiency medium SD/-Trp. The transformed AH109 mated with Y187 that contained the library plasmids via the yeast two hybridization system³. The diploid yeast cells were placed on nutrient deficiency medium SD/-Trp/-Leu/-His/-Ade and SD/-Trp/-Leu/-His/-Ade containing X- α -gal for selecting. The Blue yeast colony plasmid were extracted and electrotransformed into *E. coli* DH5 α . The plasmids in DH5 α were extracted, sequenced and blasted.

Results: The human pancreas cDNA library was constructed successfully. The reconstructed bait plasmid (pGBKT7-HCV NS4B) was transformed into yeast cells AH109 successfully. Seven proteins interacting with HCV NS4B were found.

Conclusion: Some of the seven pancreatic proteins may be related with metabolisms of glucose and lipid.

PP-132 Treatment outcome in patients with Hepatitis C: Significance of baseline parameters and viral dynamics

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Background: Hepatitis C constitutes a major public health issue around the world, especially in developing countries like Pakistan. The combination therapy with ribavirin has markedly improved the virologic response rates in hepatitis C patients. Considerable side effects and treatment costs make it desirable to identify the patients at risk of treatment failure. In this study, we investigated the prognostic significance of HCV genotyping, HCV-RNA viral load and ALT levels in the treatment outcome of patients suffering with chronic Hepatitis C infection.

Materials & Methods: Three hundred and twenty five patients with chronic HCV were enrolled. The mean age was 37.85 ± 10.03 . Personal history, serum ALT, pre treatment HCV RNA levels and genotype were quantified at the start of the treatment. Patients were treated with combination therapy of INF- α 2a (three million units thrice a week) plus ribavirin (1000–1200mg per day) for 24 weeks. HCV RNA and serum ALT level were quantified at the end of the treatment.

Results: Three hundred and eight patients completed treatment. Sustained virologic response (SVR) to therapeutic regimen was achieved in 196 (63.3%) of the patients. 54.5% were women and 45.5% were men. The SVR rate by genotypes was as follows: Genotype 3a = 66% (179 of 271), 3b = 50% (2 of 4) genotype 1a = 46.2% (6 of 13 patients), genotype 1b = 44% (4 of 9), genotype 3a+3b = 50% (4 of 8) and genotype 1a+3a = 33% (1 of 3). ALT levels

did not show any predictive significance. Best treatment response was observed in patients with genotype 3, low viral load $< 8 \times 10^5$ IU/ml and age ≤ 40 .

Conclusion: It is beneficial to include predictive variables such as HCV genotype and pretreatment quantification of viral load in the cost-benefit analysis of HCV treatment to increase the effectiveness in management of hepatitis C infection.

PP-133 High prevalence of hepatitis C infection among high risk groups in Kohgiluyeh and Boyerahmad Province, Southwest of Iran

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Objectives: Detection of HCV-infected people in each community helps the control and prevention of the infection. This study aimed to evaluate the prevalence of HCV infection among high risk groups in Kohgiluyeh and Boyerahmad province in Southwest of Iran.

Materials and Methods: This study was conducted through 2009 to 2010 in Kohgiluyeh and Boyerahmad province in Iran. High risk groups for HCV were the subjects of this study. Blood samples were taken from 2009 individuals at high risk for HCV including inmates, injecting drug users, health care workers patients on maintenance hemodialysis, hemophilic patients and patients with a history of blood transfusion from Yasuj, Gachsaran, and Dehdasht (three main townships in the province) and tested by ELISA for anti-HCV antibodies. Demographic features of participants were recorded using a questionnaire during sample collecting.

Results: Of 2009 subjects, HCV antibodies were detected in 172 (8.6%) of subjects. Rate of infection was higher in males (11.4%) compared to females (3.2%). Rate of infection in inmates was 11.7% while this rate was 42.4% in injecting drug users, 4.2% in health care workers, and 6.1% in thalassemic patients. Significant correlation was found between HCV infection and sex, marital status, history of imprisonment, drug addiction, level of education and place of residence.

Conclusion: Results of this study may help to hold back the spread of HCV infection in this and other similar settings in the region. Furthermore, findings of this study may help in improving the surveillance and prevention of the infection in the community through management and monitoring of infected individuals.

PP-134 Screening of proteins binding to hepatitis C virus NS4B protein from human pancreas cDNA library

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Aim: To screen proteins from human pancreas cDNA library, which interact with hepatitis C virus (HCV) NS4B protein.

Methods: The human pancreas cDNA library was amplified, purified and evaluated, and the purified library plasmids were transformed into yeast strain Y187. The reconstructed plasmid pGBKT7-NS4B was transformed into yeast strain AH109 and screened on the nutrient deficiency medium SD/-Trp. The transformed AH109 mated with Y187 that contained the library plasmids. The diploid yeast cells were plated on nutrient deficiency medium SD/-Trp/-Leu/-His/-Ade and SD/-Trp/-Leu/-His/-Ade containing X- α -gal for selecting. The plasmids in diploid yeast cells were extracted and electrotransformed into *E. coli* DH5 α . The plasmids in DH5 α were extracted, sequenced and blasted.